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1644

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/766,350A

DATE: 05/26/98
TIME: 09:45:47

INPUT SET: S26074.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#12 / ZR
08/26/98

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.

(ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
11D10 AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 59

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: PALO ALTO
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/766,350
(B) FILING DATE: 13-DEC-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Polizzi, Catherine M.
(B) REGISTRATION NUMBER: 40,130
(C) REFERENCE/DOCKET NUMBER: 30414-20003.21

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 813-5600
(B) TELEFAX: (650) 494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

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47         (A) LENGTH: 435 base pairs
48         (B) TYPE: nucleic acid
49         (C) STRANDEDNESS: single
50         (D) TOPOLOGY: linear
51
52     (ii) MOLECULE TYPE: DNA (genomic)
53
54
55     (ix) FEATURE:
56         (A) NAME/KEY: CDS
57         (B) LOCATION: 1..435
58
59     (ix) FEATURE:
60         (A) NAME/KEY: mat_peptide
61         (B) LOCATION: 61
62
63
64     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66     ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG CTC TTG TTT CCA      48
67     Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
68     -20                      -15                      -10                      -5
69
70     GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT      96
71     Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
72                      1                      5                      10
73
74     GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC      144
75     Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
76                      15                      20                      25
77
78     ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT      192
79     Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
80                      30                      35                      40
81
82     AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA      240
83     Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
84     45                      50                      55                      60
85
86     AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC      288
87     Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
88                      65                      70                      75
89
90     AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT      336
91     Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
92                      80                      85                      90
93
94     AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG      384
95     Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
96                      95                      100                      105
97
98     GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT      432
99     Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu

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100          110          115          120
101
102 GGG
103 Gly
104 125
105
106
107 (2) INFORMATION FOR SEQ ID NO:2:
108
109     (i) SEQUENCE CHARACTERISTICS:
110         (A) LENGTH: 145 amino acids
111         (B) TYPE: amino acid
112         (D) TOPOLOGY: linear
113
114     (ii) MOLECULE TYPE: protein
115
116     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
117
118 Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Phe Pro
119 -20          -15          -10          -5
120
121 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
122          1          5          10
123
124 Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
125          15          20          25
126
127 Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
128          30          35          40
129
130 Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
131          45          50          55          60
132
133 Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
134          65          70          75
135
136 Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
137          80          85          90
138
139 Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
140          95          100          105
141
142 Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
143          110          115          120
144
145 Gly
146 125
147
148 (2) INFORMATION FOR SEQ ID NO:3:
149
150     (i) SEQUENCE CHARACTERISTICS:
151         (A) LENGTH: 461 base pairs
152         (B) TYPE: nucleic acid

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153         (C) STRANDEDNESS: single
154         (D) TOPOLOGY: linear
155
156     (ii) MOLECULE TYPE: DNA (genomic)
157
158
159     (ix) FEATURE:
160         (A) NAME/KEY: CDS
161         (B) LOCATION: 1..459
162
163     (ix) FEATURE:
164         (A) NAME/KEY: mat_peptide
165         (B) LOCATION: 58
166
167
168     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
169
170     ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT      48
171     Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
172     -19          -15          -10          -5
173
174     GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG      96
175     Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
176           1          5          10
177
178     TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG      144
179     Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
180           15          20          25
181
182     ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG      192
183     Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
184     30          35          40          45
185
186     GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT      240
187     Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
188           50          55          60
189
190     CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC      288
191     Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
192           65          70          75
193
194     ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC      336
195     Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
196           80          85          90
197
198     TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT      384
199     Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
200           95          100          105
201
202     CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC      432
203     Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
204     110          115          120          125
205

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461

206 GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
207 Val Tyr Pro Leu Val Pro Gly Ser Leu
208 130

209
210

211 (2) INFORMATION FOR SEQ ID NO:4:

212

213 (i) SEQUENCE CHARACTERISTICS:

214 (A) LENGTH: 153 amino acids

215 (B) TYPE: amino acid

216 (D) TOPOLOGY: linear

217

218 (ii) MOLECULE TYPE: protein

219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

221

222 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
223 -19 -15 -10 -5

224

225 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
226 1 5 10

227

228 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
229 15 20 25

230

231 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
232 30 35 40 45

233

234 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
235 50 55 60

236

237 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
238 65 70 75

239

240 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
241 80 85 90

242

243 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
244 95 100 105

245

246 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
247 110 115 120 125

248

249 Val Tyr Pro Leu Val Pro Gly Ser Leu
250 130

251

252 (2) INFORMATION FOR SEQ ID NO:5:

253

254 (i) SEQUENCE CHARACTERISTICS:

255 (A) LENGTH: 321 base pairs

256 (B) TYPE: nucleic acid

257 (C) STRANDEDNESS: single

258 (D) TOPOLOGY: linear

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SEQUENCE VERIFICATION REPORT
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